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80710

From: Li, Bao-Qun
Sent: Wednesday, November 20, 2002 2:18 PM
To: STIC-Biotech/ChemLib

Please do the sequence homology and interference search of SEQ ID NO: 1 of Application SN. 09/202,035. Thank you very much. AU 1648, 8E12. ASAP.

CRF

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Class 530 subclass

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:_____	NA Sequences:_____	STN:_____
Phone:_____	AA Sequences:_1_	DIALOG:_____
Location:_____	Structures:_____	Questel/Orbit:_____
Date Picked Up:_11/22/02_	Bibliographic:_____	DRLink:_____
Date Completed:_____	Litigation:_____	Lexis/Nexis:_____
Searcher Prep/Review:_____	Full text:_____	Sequence Sys.:_DB_
Clerical:_____	Patent Family:_____	WWW/Internet:_____
Online time:_____	Other:_____	Other (specify):_____

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:
Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.
Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may requests that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpm** and **.rnpn**
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapm** and **.rapn**

The Pending database search results should not be left in the case because they contain data that is confidential.

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L2 ANSWER 1 OF 2 MEDLINE
AN 2001553895 MEDLINE
DN 21486422 PubMed ID: 11487583
TI Antiviral activity and structural characteristics of the nonglycosylated central subdomain of human respiratory syncytial virus attachment (G) glycoprotein.
AU **Gorman J J**; McKimm-Breschkin J L; Norton R S; Barnham K J
CS Biomolecular Research Institute, 343 Royal Parade, Parkville, Victoria 3052, Australia.. jeff.gorman@hsn.csiro.au
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Oct 19) 276 (42) 38988-94. Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200112
ED Entered STN: 20011016
Last Updated on STN: 20020122
Entered Medline: 20011204
AB Segments of the cystine noose-containing nonglycosylated central subdomain, residues 149-197, of the attachment (G) glycoprotein of human respiratory syncytial virus (HRSV) have been assessed for impact on the cytopathic effect (CPE) of respiratory syncytial virus (**RSV**). Nalpha-acetyl residues 149-197-amide (G149-197), G149-189, and G149-177 of the A2 strain of HRSV protected 50% of human epithelial HEp-2 cells from the CPE of the A2 strain at concentrations (IC(50)) between 5 and 80 microm. Cystine noose-containing peptides G171-197 and G173-197 did not inhibit the CPE even at concentrations above 150 microm. Systematic C- and N-terminal truncations from G149-189 and G149-177 and alanine substitutions within G154-177 demonstrated that residues 166-170 (EVFNF), within a sequence that is conserved in HRSV strains, were critical for inhibition. Concordantly, G154-177 of bovine **RSV** and of an antibody escape mutant of HRSV with residues 166-170 of QTLPY and EVSNP, respectively, were not inhibitory. Surprisingly, a variant of G154-177 with an E166A substitution had an IC(50) of 750 nm. NMR analysis demonstrated that G149-177 adopted a well-defined conformation in solution, clustered around F168 and F170. G154-170, particularly EVFNF, may be important in binding of **RSV** to host cells. These findings constitute a promising platform for the development of antiviral agents for **RSV**.
CT Check Tags: Animal; Human
Alanine: CH, chemistry
Amino Acid Sequence
*Antiviral Agents: PD, pharmacology
Cattle
Glycosylation
Inhibitory Concentration 50
Magnetic Resonance Spectroscopy
*Membrane Glycoproteins: CH, chemistry
Models, Molecular
Molecular Sequence Data
Mutagenesis, Site-Directed
Peptides: CH, chemistry
*Peptides: PD, pharmacology
Protein Binding
Protein Conformation
Protein Structure, Tertiary
*Respiratory Syncytial Virus, Human: CH, chemistry
Sequence Homology, Amino Acid
Sheep

*Viral Envelope Proteins: CH, chemistry
RN 56-41-7 (Alanine)
CN 0 (Antiviral Agents); 0 (G protein, bovine respiratory syncytial virus); 0 (Membrane Glycoproteins); 0 (Peptides); 0 (Viral Envelope Proteins); 0 (glycoprotein O, human respiratory syncytial virus)

L2 ANSWER 2 OF 2 MEDLINE
AN 97337451 MEDLINE
DN 97337451 PubMed ID: 9194191
TI Determination of the disulfide bond arrangement of human respiratory syncytial virus attachment (G) protein by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry.
AU **Gorman J J**; Ferguson B L; Speelman D; Mills J
CS Biomolecular Research Institute, Parkville, Vic., Australia.. jeff.gorman@bioresi.corn.au
SO PROTEIN SCIENCE, (1997 Jun) 6 (6) 1308-15.
Journal code: 9211750. ISSN: 0961-8368.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199708
ED Entered STN: 19970825
Last Updated on STN: 20000303
Entered Medline: 19970813
AB The attachment protein or G protein of the A2 strain of human respiratory syncytial virus (**RSV**) was digested with trypsin and the resultant peptides separated by reverse-phase high-performance liquid chromatography (HPLC). One tryptic peptide produced a mass by matrix-assisted laser desorption/ionization (MALDI) time-of-flight (TOF) mass spectrometry (MS) corresponding to residues 152-187 with the four Cys residues of the ectodomain (residues 173, 176, 182, and 186) in disulfide linkage and absence of glycosylation. Sub-digestion of this tryptic peptide with pepsin and thermolysin produced peptides consistent with disulfide bonds between Cys173 and Cys186 and between Cys176 and Cys182. Analysis of ions produced by post-source decay of a peptic peptide during MALDI-TOF-MS revealed fragmentation of peptide bonds with minimal fission of an inter-chain disulfide bond. Ions produced by this unprecedented MALDI-induced post-source fragmentation corroborated the existence of the disulfide arrangement deduced from mass analysis of proteolysis products. These findings indicate that the ectodomain of the G protein has a non-glycosylated subdomain containing a "cystine noose."
CT Check Tags: Support, Non-U.S. Gov't
Amino Acid Sequence
*Cystine: CH, chemistry
*Disulfides: CH, chemistry
Molecular Sequence Data
Peptide Fragments: CH, chemistry
Sequence Analysis: MT, methods
Spectrometry, Mass, Matrix-Assisted Laser Desorption-Ionization
*Viral Proteins: CH, chemistry
RN 56-89-3 (Cystine)
CN 0 (Disulfides); 0 (Peptide Fragments); 0 (Viral Proteins); 0 (attachment protein G); 0 (respiratory syncytial virus proteins)